

# SEQUENCE LISTING

78-0B10 amino acid sequence (SEQ ID NO:1)

5	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
	1				5					10					15	
	Ala	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
			20						25				30			
	Ala	Asp	Ile	Ser	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
			35					40					45			
10	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
	50						55					60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
	65				70						75				80	
	Ser	Glu	Asn	Gly	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
				85						90					95	
15	Leu	Gly	Ile	Ile	Ala	Ala	Pro	Val	Ser	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
			100						105					110		
	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Ile	Phe	Cys	Ser
		115						120					125			
20	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
	130					135						140				
	Val	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr
	145				150						155				160	
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165						170					175	
25	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
			180						185					190		
	Leu	Val	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Val	Pro	Lys	Gly	Val	Met
	195						200					205				
30	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Leu	Ala	Lys	Asp	Pro
	210					215						220				
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Thr	Ala	Ile	Leu	Thr	Val	Ile
	225				230						235				240	
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
				245						250				255		
35	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
			260						265					270		
	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
	275						280					285				
40	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
	290					295					300					
	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys
	305				310						315				320	
	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg
				325						330				335		
45	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro
			340					345					350			
	Lys	Gly	Asp	Ala	Arg	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Phe	His
		355					360					365				
50	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn
	370					375						380				
	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Ala	Met	Ile	Met	Lys	Gly	Tyr
	385				390					395					400	
	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp
55				405					410					415		

	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr
				420					425					430		
	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val
			435					440					445			
5	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val
		450					455					460				
	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Ala	Gly	Glu	Leu	Pro
	465					470					475					480
	Ala	Ala	Gly	Val	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile
10					485					490					495	
	Val	Gln	Asp	Phe	Val	Ser	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg
			500					505						510		
	Gly	Gly	Val	Lys	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys
			515					520					525			
15	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Phe	Glu	Lys	His	Thr	Asn	Gly
		530					535					540				

90-1B5 amino acid sequence (SEQ ID NO:2)

20	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
	1				5					10					15	
	Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
				20					25					30		
25	Ala	Asp	Ile	Pro	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
			35					40					45			
	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
		50					55					60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
30	65					70					75				80	
	Ser	Glu	Asn	Gly	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
				85						90					95	
	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
			100						105					110		
35	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser
			115					120					125			
	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
		130					135					140				
	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr
40	145					150					155					160
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165						170					175	
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
				180					185					190		
45	Leu	Ile	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Met
			195					200					205			
	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Leu	Ala	Lys	Asp	Pro
		210					215					220				
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Thr	Ala	Ile	Leu	Thr	Val	Ile
50	225					230					235				240	
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
				245						250					255	
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
				260					265					270		
55	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
		275						280					285			
	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
		290					295					300				

	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys
	305					310					315					320
	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg
					325					330					335	
5	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro
				340					345					350		
	Lys	Gly	Asp	Ala	Lys	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Phe	His
		355						360					365			
10	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn
		370					375					380				
	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Pro	Met	Ile	Met	Lys	Gly	Tyr
	385					390				395						400
	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp
				405						410					415	
15	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr
				420					425					430		
	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val
			435					440					445			
20	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val
		450					455					460				
	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Ala	Gly	Glu	Leu	Pro
	465					470				475						480
	Ala	Ala	Gly	Val	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile
				485						490					495	
25	Val	Gln	Asp	Tyr	Val	Ala	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg
			500						505					510		
	Gly	Gly	Val	Lys	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys
			515					520					525			
30	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Phe	Glu	Lys	His	Thr	Asn	Gly
		530					535					540				

133-1B2 amino acid sequence (SEQ ID NO:3)

35	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
	1				5					10					15	
	Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
				20					25					30		
40	Ala	Asp	Ile	Pro	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
			35				40						45			
	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
		50					55					60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
	65				70					75					80	
45	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
				85						90					95	
	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
			100						105					110		
50	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser
			115				120						125			
	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
		130					135					140				
	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Asp	Asp	Leu	Gly	Gly	Tyr
	145					150					155					160
55	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165						170				175		
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
				180					185					190		

5 Leu Ile Met Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met  
 195 200 205  
 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Ile Ala Lys Asp Pro  
 210 215 220  
 Thr Phe Gly Asn Ala Ile Asn Pro Thr Ser Ala Ile Leu Thr Val Ile  
 225 230 235 240  
 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr  
 245 250 255  
 10 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe  
 260 265 270  
 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Val Pro  
 275 280 285  
 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp  
 290 295 300  
 15 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys  
 305 310 315 320  
 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg  
 325 330 335  
 20 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro  
 340 345 350  
 Lys Gly Asp Ala Lys Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His  
 355 360 365  
 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn  
 370 375 380  
 25 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Pro Met Ile Met Lys Gly Tyr  
 385 390 395 400  
 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Asp Asn Asp Gly Trp  
 405 410 415  
 30 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr  
 420 425 430  
 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val  
 435 440 445  
 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val  
 450 455 460  
 35 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro  
 465 470 475 480  
 Ala Ala Gly Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile  
 485 490 495  
 40 Val Gln Asp Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg  
 500 505 510  
 Gly Gly Val Ile Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys  
 515 520 525  
 Ile Asp Arg Lys Val Leu Arg Gln Met Leu Glu Lys His Thr Asn Gly  
 530 535 540  
 45

146-1H2 amino acid sequence (SEQ ID NO:4)

50 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu  
 1 5 10 15  
 Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr  
 20 25 30  
 Ala Ala Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu  
 35 40 45  
 55 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu  
 50 55 60  
 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys  
 65 70 75 80

	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr	
					85					90						95	
	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu	
				100					105					110			
5	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser	
			115					120					125				
	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser	
		130					135					140					
	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr	
10	145					150				155						160	
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp	
				165					170					175			
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala	
				180					185					190			
15	Ser	Ile	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Met	
			195					200					205				
	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Ile	Ala	Lys	Asp	Pro	
		210				215						220					
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Ser	Ala	Ile	Leu	Thr	Val	Ile	
20	225					230					235					240	
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr	
				245						250					255		
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe	
				260				265						270			
25	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro	
			275				280						285				
	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp	
		290				295						300					
	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys	
30	305				310					315					320		
	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg	
				325						330					335		
	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro	
				340					345					350			
35	Lys	Gly	Asp	Ala	Lys	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Leu	His	
		355					360						365				
	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn	
		370				375						380					
	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Pro	Met	Ile	Met	Lys	Gly	Tyr	
40	385				390					395					400		
	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp	
				405					410					415			
	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr	
				420				425					430				
45	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val	
		435					440						445				
	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val	
		450				455						460					
	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Ala	Gly	Glu	Leu	Pro	
50	465				470					475					480		
	Ala	Ala	Gly	Val	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile	
				485					490					495			
	Val	Gln	Asp	Tyr	Val	Ala	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg	
			500					505					510				
55	Gly	Gly	Val	Lys	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys	
			515				520					525					
	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Leu	Glu	Lys	His	Thr	Asn	Gly	
				530			535					540					

73-0E10 (SEQ ID NO:5)

5 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGGTG  
ATGGGACGGGTGGAGAACAGATSTTTGACGCATTATCTCGTTATGCAGATATTTCCCGA  
TGCATAGCATTGACAAATGCTCATAACAAAAGAAAATGTTTTATATGAAGAGTTTTTAAA  
ATTGTCTGTCTGTTTAGCGGAAAGTTTTAAAAAGTATGSAATAAAACAAAACGACACAA  
TAGCGGTGTGTAGCGAAAATGGTTTGCAATTTTTCTTCTGTAAATGCATCATTGTAT  
CTTGAATAATTGCAGCACCTGTTAGTGATAAATACATTGAACGTGAATTAATACACAG  
TCTTGGTATTGTAAAACACGACATAATTTTTTGTCCAAGAATACTTTTCAAAAAGTAC  
10 TGAATGTAAAATCTAAATTAATAATCTGTAGAAAATATTATTATATTAGACTTAAATGAA  
GACTTAGGAGSTTATCAATGGCTCAACAACCTTTATTTCTCAAAATTCGGATAGTAATCT  
GGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGTAA  
TGTTTTCTTCTGGTACAACTGGTGTTCGGAAGGGAGTCATGCTAACTCACAAGAAATTT  
GTTGCACGATTTTCTCTTGCAAAAGATCCTACTTTTGGTAACGCAATTAATCCACGAC  
15 AGCAATTTTAACGGTAATACCTTTCCACCATGGTTTTGGTATGATGACCACATTAGGAT  
ACTTTACTTGTGGATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAAACTATTCTA  
CAATCATTACAAGATTATAAAGTGGAAAGTACTTTACTTGTACCAACATTAATGGCATT  
TCTTGCAAAAAGTGCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTCAT  
CTGGTGGCGCACCTTTATCAAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTTAAATTA  
20 AACTTTGTGAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTAATTACACC  
GAAAGGTGACGCCAGACCGGGATCAACTGGTAAAATAGTACCATTTACGCTGTAAAG  
TTGTGATCCTACAACAGGAAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTT  
AAAGGCGCCATGATAATGAAGGGTTATTATAATAATGAAGAAGCTACTAAAGCAATPAT  
TGATAATGACGGATGGTTGCGCTCTGGTGATATTGCTTATTATGACAATGATGGCCATT  
25 TTTATATTGTGGACAGGCTGAAGTCATTAATTAATATAAAGGTTATCAGGTTGCACCT  
GCTGAAATTGAGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGG  
TATACCGGATGAAGCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAA  
AATATCTAAACGAACAAATCGTACAAGATTTTGTTCAGTCAAGTTTCAACAGCAAAA  
TGGCTACGTGGTGGGGTGAAATTTTTGGATGAAATTCCTCAAAGGATCAACTGGAAAAAT  
30 TGACAGAAAAGTGTTAAGACAAATGTTTGAAAAACACACCAATGGG

98-1E5 (SEQ ID NO:6)

5 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGGAGA  
TGGGACGGGTGGAGAACAGATSTTTGACGCATTATCTCGTTATGCAGATATTCGGGGGTG  
35 CATAGCATTGACAAATGCTCATAACAAAAGAAAATGTTTTATATGAAGAGTTTTGTAACT  
GTCGTGTCTGTTTAGCGGAAAGTTTTAAAAAGTATGSAATAAAACAAAACGACACAATAGC  
GGTGTGTAGCGAAAATGGTCTGCAATTTTTCTTCTGTAAATGCATCATTGTATCTTGG  
AATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGG  
TATTGTAAAACACGACATAGTTTTTTGTCCAAGAATACTTTTCAAAAAGTACTGAATGT  
40 AAAATCTAAATTAATAATCTATTGAACTATTATTATATTAGACTTAAATGAAGACTTAGG  
AGGTTATCAATGGCTCAACAACCTTTATTTCTCAAAATTCGATAGTAATCTGGACGTAA  
AAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGATTATGTTTTCTTC  
TGTACAACTGGTCTGCGGAAGGGAGTCATGCTAACTCACAAGAAATATTGTTGCAGGATT  
TTCTCTTGCAAAAAGATCCTACTTTTGGTAACGCAATTAATCCACGACAGCAATTTTAA  
45 GGTAATACCTTTCCACCATGGTTTTTGGTATGATGACCACATTACGATACTTTACTTGTGG  
ATTCCGAGTGTCTTAATGCACACGTTTGAAGAAAAACTATTCTACAAATCATTACAAGA  
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ATTACTTGAAAAGTACGATTTATCGCACTTAAAAGAAATGCAATCTGGTGGGCACTTTT  
ATCAAAAAGAAATTGGGGAGATGGTGAAAAAACGTTTTAAATTAACCTTTGTGAGCAAGG  
50 STATGGATTAACAGAAACCACTTCGGCTGTTTTTAATTACACCGAAAGGTGAGGCCAAAC  
GGGATCAACTGTTAAAATAGTACCACTTTCAAGCTGTAAASTTGTGATCTTACAACAGG  
AAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTTAAAGGCGCGATGATAATGAA  
1200

	GGTTATTATAATAATGAAGAACTACTAAAGCAATTATTGATAATGACGGATGGTTGGG	1280
	CTGTGGTGATATTGCTTATTATGACAAATGATGGCCATTTTATATTGTGGACAGGCTGAA	1320
	GTCACTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAGGGAATACTCTT	1360
	ACAAACATCCGTATATTGTTGATGCCGGGCTTACTGGTATACCGGATGAAGCCGGGGGA	1400
5	GCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAAAAATATCTAAACGAACAAATCGTACA	1440
	AGATTATGTTGCCAGTCAAGTTTCAACAGCCAAATGGCTACCTGGTGGGTCGAAATTTTT	1480
	GGATGAAATTCCCAAAGGATCAACTGGAAAAATTGACAGAAAAAGTGTTAAGACAAATGTT	1520
	TGAAAAACACACCAATGGG	1560

10 133-1B2 (SEQ ID NO:7)

	AGATCCCAATGGCAGATAAGAATATTTTATATGGGCCCGAACCATTTTATCCCTTGGAAAG
	ATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATATTCCGGGC
	TGCATAGCATTGACAAATGCTCATACAAAAGAAAAATGTTTTATATGAAGAGTTTCTGAA
	ACTGTCTGTGTGTTTAGCGGAAAGTTTTAAAAAGTATGGATTAAAAACAAAACGACACAA
15	TAGCGGTGTGTAGCGAAAATAGTCTGCAATTTTTCTTCTCTGTAATTGCATCATTGTAT
	CTTGGAAATAATTGTGGCACCTGTTAACGATAAAATACATTGAACGTGAATTAATACACAG
	TCTTGSTATTGTAAAACCAAGCATAGTTTTTTTGCTCCAAGAATACTTTTCAAAAAGTAC
	TGAATGTAAAATCTAAATTAAAAATCTATTGAAACTATTATTATATTAGACTTAAATGAT
	GACTTAGGAGGTTATCAATGGCTCAACAACCTTTATTTCTCAAAAATTCGGATAGTAATCT
20	GGACGTAAAAAAATTTAAACCATATTTCTTTAATCGAGACGATCAGGTTGCGTTGATTA
	TGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCTAACCTCACAAGAATATT
	GTTGCACGATTTTCTATTGCAAAAAGATCCTACTTTTGGTAACGCAATTAATCCACGCTC
	AGCAATTTTAAACGGTAATACCTTTCCACCATGGTTTTGGTATGATGACCACATTAGGAT
	ACTTTACTTGTGGATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAACTATTCTTA
25	CAATCATTACAAGATTATAAAGTGGAAAGTACTTTACTTGTACCAACATTAAATGSCATT
	TCTTGCAAAAAGTGCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCAT
	CTGGTGGCGCACCTTTATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
	AACTTTGTCAAGGCAAGGGTATGGATTAAACAGAAACCACTTCGGCTGTTTTAATTACACC
	GAAAGGTGACGCCAAACCGGGATCAACTGGTAAAATAGTACCATTTACCGCTGTTAAAG
30	TTGTGATCCTACAACAGGAAAAATTTGGGGCCAAATGAACCTGGAGAATTGATTTTT
	AAAGGCCCGATGATAATGAAGGGTTATTATAAATGAAGAAGCTACTAAAGCAATTAT
	TGATAATGACGGATGGTTGCGCTCTGGTGATATTGCTTATTATGACAATGATGGCCATT
	TTTATATTGTGGACAGGCTGAAGTCACTGATTAAATATAAAGGTTATCAGGTTGCACCT
	GCTGAAATTGAGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGG
35	TATACCGGATGAAGCCCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAA
	AATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTCAAAAGGAAAA
	TGGCTACGTGGTGGGGTGATATTTTTGGATGAAATTCCCAAAGGATCAACTGGAAAAAT
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40 146-1H2 (SEQ ID NO:8)

	GGATCCCAATGGCAGATAAGAATATTTTATATGGGCCCGAACCATTTTATCCCTTGGAAAG
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	TGCATAGCATTGACAAATGCTCATACAAAAGAAAAATGTTTTATATGAAGAGTTTCTGAA
	ACTGTCTGTGTGTTTAGCGGAAAGTTTTAAAAAGTATGGATTAAAAACAAAACGACACAA
45	TAGCGGTGTGTAGCGAAAATAGTCTGCAATTTTTCTTCTCTGTAATTGCATCATTGTAT
	CTTGGAAATAATTGTGGCACCTGTTAACGATAAAATACATTGAACGTGAATTAATACACAG
	TCTTGSTATTGTAAAACCAAGCATAGTTTTTTTGCTCCAAGAATACTTTTCAAAAAGTAC
	TGAATGTAAAATCTAAATTAAAAATCTATTGAAACTATTATTATATTAGACTTAAATGAA
	GACTTAGGAGGTTATCAATGGCTCAACAACCTTTATTTCTCAAAAATTCGGATAGTAATCT
50	GGACGTAAAAAAATTTAAACCTATTCTTTTAAATCGAGACGATCAGGTTGCGTCGATTA

5

10

15

20

TGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCTAACTCACAAGAATATT  
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